



SEQUENCE LISTING

<110> MACK, DAVID
GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER,
COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST
CANCER MODULATORS

<130> A-67860-3/DJB/JJD

<140> US 09/525,361

<141> 2000-03-15

<150> US 09/268,865

<151> 1999-03-15

<150> US 09/450,810

<151> 1999-11-29

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<151> 1999-12-02

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<170> PatentIn Ver. 2.1

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APR 18 2001

TECH CENTER 1600/2900

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Asn Lys Phe Leu Arg Pro Asn Phe Gly Gly Glu Pro Val Gln Ile Ala
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Leu Thr Leu Asp Ile Ala Ser Ile Ser Ser Ile Ser Glu Ser Asn Met
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Asp Tyr Thr Ala Thr Ile Tyr Leu Arg Gln Arg Trp Met Asp Gln Arg
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Glu Phe Leu Trp Val Pro Asp Thr Tyr Ile Val Glu Ser Lys Lys Ser
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Asn Gly Thr Val Leu Tyr Ala Leu Arg Ile Thr Thr Thr Val Ala Cys
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Glu Thr Gly Asn Tyr Thr Arg Leu Val Leu Gln Phe Glu Leu Arg Arg
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Ala Ile Asp Val Tyr Leu Gly Ile Cys Phe Ser Phe Val Phe Gly Ala
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Leu Leu Glu Tyr Ala Val Ala His Tyr Ser Ser Leu Gln Gln Met Ala
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Ala Ser Ile Glu Ile Ser Ser Asp Asn Val Asp Tyr Ser Asp Leu Thr
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Met Lys Thr Ser Asp Lys Phe Lys Phe Val Phe Arg Glu Lys Met Gly
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Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
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Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
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Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe
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Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro
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Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met
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Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
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Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys
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Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu
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Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn
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Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg
 385 390 395 400

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Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg
420 425 430

Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu
435 440 445

Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Asp
450 455 460

Glu Lys Glu Val Gly Lys Glu Ala Asn Glu Asn Glu Thr Asn Gln Ser
465 470 475 480

Glu Ser His Val Lys Pro Ser Gln Arg Phe Glu Phe
485 490

<210> 9
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 9
Cys Lys Pro Asp Thr Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr
1 5 10 15

<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 10
Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val Glu Tyr Cys
1 5 10 15

<210> 11
<211> 1958

<212> DNA

<213> Homo sapiens

<400> 11

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aaccaggtat tctaaacttg aaaaaaaaaa aaaaaaaaaa 1958
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<210> 12

<211> 582

<212> DNA

<213> Homo sapiens

<400> 12

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cacggccaga cgtcctcgct gtgggtggaa tgctcccaag agggcggcgg cagcgggtcc 180
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<210> 13

<211> 193

<212> PRT

<213> Homo sapiens

<400> 13

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
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20 25 30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45

Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
100 105 110

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
115 120 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
130 135 140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175

Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190

Ala

<210> 14
<211> 193
<212> PRT
<213> Mouse

<400> 14

Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
1 5 10 15

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20 25 30

Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
35 40 45

Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
65 70 75 80

Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
85 90 95

Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
100 105 110

Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
115 120 125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
130 135 140

Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160

Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175

Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
180 185 190

Ala

<210> 15
<211> 124
<212> PRT
<213> Rat

<400> 15

Glu Tyr Ala Trp Gly Arg Ala Ala Ala Thr Leu Phe Cys Gly Phe
1 5 10 15

Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly
20 25 30

Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
35 40 45

Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
50 55 60

Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
65 70 75 80

Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
85 90 95

Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu
100 105 110

Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
115 120

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 16

Cys Ser Tyr Ser Ala Pro Ser Pro Ser Thr Ser Ser Arg Trp Pro
1 5 10 15

<210> 17
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 17
 Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro
 1 5 10 15

<210> 18
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 18
 Cys Gly Gly Asn Ala Pro Lys Arg Gly Gly Gly Arg Gly Ser Tyr
 1 5 10 15

<210> 19
 <211> 1970
 <212> DNA
 <213> Mouse

<400> 19
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 ggccgctgct cctgcccggc gtctctccgc tccgcgcccg ccgccaccga cgacatgctg 180
 cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc cctgctgct gctcagcgcc 240
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 tgggcaatgt tcatatgatc agaaatgtta gaataaatgc taaagaaaat tcttcataat 900

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<210> 20

<211> 582

<212> DNA

<213> Mouse

<400> 20

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cacatccaga catcgctcgt ttgggtggagg tgtttcgacg agggcggcgg cagcggtctc 180
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atcatcttga ttggttggtc cttcttcttc tgctgcctcc ccaactacga ggatgacctt 540
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<210> 21

<211> 536

<212> DNA

<213> Rat

<400> 21

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gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct gggtatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240

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aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
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 tatacatctg cctaattgtg agggagatcc tgagaaaagc ctgctgcaag atgcatgtga 420
 ggaggaaagt gttctccaag gagcaaagaa cctatgtttg ggcagtgttc atatgagtgg 480
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<210> 22

<211> 375

<212> DNA

<213> Rat

<400> 22

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 aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctctttcttc 300
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<210> 23

<211> 471

<212> DNA

<213> Homo sapiens

<400> 23

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 ttcattgcttc ctgtgatttc atccaactac ttaccttgcc tacgatatcc cctttatctc 420
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<210> 24

<211> 273

<212> DNA

<213> Homo sapiens

<400> 24

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 gccctgatg ctgaaaccac tgctgctgca accactgcga ccaactgctgc tctaccact 180
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273

<210> 25

<211> 90

<212> PRT

<213> Homo sapiens

<400> 25

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

<210> 26

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 26

Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
1 5 10 15

<210> 27

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 27

Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
1 5 10 15

<210> 28

<211> 1555

<212> DNA

<213> Homo sapiens

<400> 28

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<210> 29

<211> 291

<212> PRT

<213> Homo sapiens

<400> 29

Met Thr Asn Asp Ser Glu Gly Lys Met Gly Phe Lys His Pro Lys Ile
1 5 10 15

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Gly | Asn | Phe | Arg | Gly | His | Ala | Leu | Pro | Gly | Thr | Phe | Phe | Phe | Ile | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Ile | Gly | Leu | Trp | Trp | Cys | Thr | Lys | Ser | Ile | Leu | Lys | Tyr | Ile | Cys | Lys | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | |
| Lys | Gln | Lys | Arg | Thr | Cys | Tyr | Leu | Gly | Ser | Lys | Thr | Leu | Phe | Tyr | Arg | | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | | |
| Leu | Glu | Ile | Leu | Glu | Gly | Ile | Thr | Ile | Val | Gly | Met | Ala | Leu | Thr | Gly | | | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | | | |
| Met | Ala | Gly | Glu | Gln | Phe | Ile | Pro | Gly | Gly | Pro | His | Leu | Met | Leu | Tyr | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Asp | Tyr | Lys | Gln | Gly | His | Trp | Asn | Gln | Leu | Leu | Gly | Trp | His | His | Phe | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| Thr | Met | Tyr | Phe | Phe | Phe | Gly | Leu | Leu | Gly | Val | Ala | Asp | Ile | Leu | Cys | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | |
| Phe | Thr | Ile | Ser | Ser | Leu | Pro | Val | Ser | Leu | Thr | Lys | Leu | Met | Leu | Ser | | | |
| | | 130 | | | | 135 | | | | | 140 | | | | | | | |
| Asn | Ala | Leu | Phe | Val | Glu | Ala | Phe | Ile | Phe | Tyr | Asn | His | Thr | His | Gly | | | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | | | |
| Arg | Glu | Met | Leu | Asp | Ile | Phe | Val | His | Gln | Leu | Leu | Val | Leu | Val | Val | | | |
| | | | 165 | | | | | | 170 | | | | | 175 | | | | |
| Phe | Leu | Thr | Gly | Leu | Val | Ala | Phe | Leu | Glu | Phe | Leu | Val | Arg | Asn | Asn | | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | | |
| Val | Leu | Leu | Glu | Leu | Leu | Arg | Ser | Ser | Leu | Ile | Leu | Leu | Gln | Gly | Ser | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | |
| Trp | Phe | Phe | Gln | Ile | Gly | Phe | Val | Leu | Tyr | Pro | Pro | Ser | Gly | Gly | Pro | | | |
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Glu Glu Met
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Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
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Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
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<212> DNA

<213> Homo sapiens

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Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
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Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
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<210> 38

<211> 392

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (111)

<223> "Xaa" at position 111 can be any amino acid.

<400> 38

Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
1 5 10 15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
20 25 30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
35 40 45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
50 55 60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
65 70 75 80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
85 90 95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
100 105 110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
115 120 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
130 135 140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145 150 155 160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
165 170 175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
180 185 190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
195 200 205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
210 215 220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225 230 235 240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
245 250 255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
 260 265 270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
 275 280 285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
 290 295 300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
 305 310 315 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
 325 330 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
 340 345 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
 355 360 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
 370 375 380

Ser Arg Phe Leu Arg Pro Tyr Lys
 385 390

<210> 39
 <211> 392
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (111)
 <223> "Xaa" at position 111 can be any amino acid.

<400> 39
 Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
 1 5 10 15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
 20 25 30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
 35 40 45

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Cys | Pro | Asn | Gly | Thr | Phe | Gln | Asn | Glu | Glu | Gly | Gln | Met | Thr | Cys | 50 | 55 | 60 | |
| Glu | Pro | Cys | Pro | Arg | Pro | Gly | Asn | Ser | Gly | Ala | Leu | Lys | Thr | Pro | Glu | 65 | 70 | 75 | 80 |
| Ala | Trp | Asn | Met | Ser | Glu | Cys | Gly | Gly | Leu | Cys | Gln | Pro | Thr | Glu | Tyr | 85 | 90 | 95 | |
| Ser | Ala | Asp | Gly | Phe | Ala | Pro | Cys | Gln | Leu | Cys | Ala | Leu | Gly | Xaa | Phe | 100 | 105 | 110 | |
| Gln | Pro | Glu | Ala | Gly | Arg | Thr | Ser | Cys | Phe | Pro | Cys | Gly | Gly | Gly | Leu | 115 | 120 | 125 | |
| Ala | Thr | Lys | His | Gln | Gly | Ala | Thr | Ser | Phe | Gln | Asp | Cys | Glu | Thr | Arg | 130 | 135 | 140 | |
| Val | Gln | Cys | Ser | Pro | Gly | His | Phe | Tyr | Asn | Thr | Thr | Thr | His | Arg | Cys | 145 | 150 | 155 | 160 |
| Ile | Arg | Cys | Pro | Val | Gly | Thr | Tyr | Gln | Pro | Glu | Phe | Gly | Lys | Asn | Asn | 165 | 170 | 175 | |
| Cys | Val | Ser | Cys | Pro | Gly | Asn | Thr | Thr | Thr | Asp | Phe | Asp | Gly | Ser | Thr | 180 | 185 | 190 | |
| Asn | Ile | Thr | Gln | Cys | Lys | Asn | Arg | Arg | Cys | Gly | Gly | Glu | Leu | Gly | Asp | 195 | 200 | 205 | |
| Phe | Thr | Gly | Tyr | Ile | Glu | Ser | Pro | Asn | Tyr | Pro | Gly | Asn | Tyr | Pro | Ala | 210 | 215 | 220 | |
| Asn | Thr | Glu | Cys | Thr | Trp | Thr | Ile | Asn | Pro | Pro | Pro | Lys | Arg | Arg | Ile | 225 | 230 | 235 | 240 |
| Leu | Ile | Val | Val | Pro | Glu | Ile | Phe | Leu | Pro | Ile | Glu | Asp | Asp | Cys | Gly | 245 | 250 | 255 | |
| Asp | Tyr | Leu | Val | Met | Arg | Lys | Thr | Ser | Ser | Ser | Asn | Ser | Val | Thr | Thr | 260 | 265 | 270 | |
| Tyr | Glu | Thr | Cys | Gln | Thr | Tyr | Glu | Arg | Pro | Ile | Ala | Phe | Thr | Ser | Arg | 275 | 280 | 285 | |
| Ser | Lys | Lys | Leu | Trp | Ile | Gln | Phe | Lys | Ser | Asn | Glu | Gly | Asn | Ser | Ala | 290 | 295 | 300 | |

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305 310 315 320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
325 330 335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
340 345 350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
355 360 365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
370 375 380

Ser Arg Phe Leu Arg Pro Tyr Lys
385 390

<210> 40
<211> 162
<212> PRT
<213> Mouse

<400> 40
Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile Leu Ile Val Val Pro Glu
1 5 10 15

Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu Val Met Arg
20 25 30

Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr
35 40 45

Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile
50 55 60

Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
65 70 75 80

Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
85 90 95

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
100 105 110

Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln

115

120

125

Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met Phe Pro Arg
 130 135 140

Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu Arg Pro
 145 150 155 160

Tyr Lys

<210> 41

<211> 2840

<212> DNA

<213> Homo sapiens

<400> 41

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 tcacaccaga catgatggt caggaaaggc ctcttgatgt tgactgtaaa cgcctaagcc 780
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 gaaaatataa tgtttttaag aaggaacagt agtggaatga atgttaaaag atctttatgt 1800

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tgtcaagaaa gcagaaacca tctcatttct aacagctgtg ttatattcca tagtatgat 2760
tactcaacaa actgttgtgc tattggatac ttaggtggtt tcttactga caatactgaa 2820
taaacatctc accggaattc                                     2840

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<210> 42

<211> 1041

<212> DNA

<213> Homo sapiens

<400> 42

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cggatgccca accacctgca ccacagcacg caggagaacg ccattcctggc catcgagcag 180
tacgaggagc tgggtggacgt gaactgcagc gccgtgtgtc gcttcttctt ctgtgccatg 240
tacgcgcccc tttgcaccct ggagttcctg cagcacccta tcaagccgtg caagtcggtg 300
tgccaacgcg cgcgcgacga ctgcgagccc ctcatgaaga tgtacaacca cagctggccc 360
gaaagcctgg cctgcgacga gctgcctgtc tatgaccgtg gcgtgtgcat ttcgcctgaa 420
gccatcgtca cggacctccc ggaggatggt aagtggatag acatcacacc agacatgatg 480
gtacaggaaa ggctcttga tgttgactgt aaacgccta gccccgatcg gtgcaagtgt 540
aaaaagggtg agccaacttt ggcaacgtat ctacgcaaaa actacagcta tgttattcat 600
gcaaaaataa aagctgtgca gaggagtggc tgcaatgagg tcacaacggg ggtggatgta 660
aaagagatct tcaagtcctc atcaccatc cctcgaactc aagtcccgtt cattacaaat 720
tcttcttgcc agtgtccaca catcctgccc catcaagatg ttctcatcat gtgttacgag 780
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agtaaaagat ccatacagtg ggaagagagg ctgcaggaac agcggagAAC agttcaggac 900
aagaagaaaa cagccggggc caccagtcgt agtaatcccc ccaaaccaaa gggaaagcct 960
cctgctccca aaccagccag tccaagaag aacattaaaa ctaggagtgc ccagaagaga 1020
acaaaccgca aaagagtgtg a                                     1041

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<210> 43

<211> 346

<212> PRT

<213> Homo sapiens

<400> 43

Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
1 5 10 15

Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
20 25 30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
35 40 45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
50 55 60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
65 70 75 80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
85 90 95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
100 105 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
115 120 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
130 135 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145 150 155 160

Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
165 170 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
180 185 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
195 200 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
210 215 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
225 230 235 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
 245 250 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
 260 265 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
 275 280 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
 290 295 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
 305 310 315 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
 325 330 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
 340 345

<210> 44

<211> 749

<212> DNA

<213> Homo sapiens

<400> 44

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 gcaataaaaa aggaaaagag gcctcctcag acactctcaa gaggatgggg agatgacatc 180
 acttgggtac aaacttatga agaaggtctc ttttatgctc aaaaaagtaa gaagccatta 240
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 caaatgaag aaatacaaga aatggctcag aataagttca tcatgctaaa ccttatgcat 360
 gaaaccactg ataagaattt atcacctgat gggcaatatg tgcctagaat catgtttgta 420
 gacccttctt taacagttag agctgacata gctggaagat actctaacag attgtacaca 480
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 gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgaata 660
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<210> 45

<211> 501

<212> DNA

<213> Homo sapiens

<400> 45

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ccattaatgg ttattcatca cctggaggat tgtcaatact ctcaagcact aaagaaagta 240
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cttattcagt cagagctata a                                     501
```

<210> 46

<211> 166

<212> PRT

<213> Homo sapiens

<400> 46

```
Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr Val
  1                      5                      10                      15
```

```
Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
          20                      25                      30
```

```
Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
      35                      40                      45
```

```
Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
      50                      55                      60
```

```
Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
      65                      70                      75                      80
```

```
Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
          85                      90                      95
```

```
Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
      100                      105                      110
```

```
Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
      115                      120                      125
```

```
Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
      130                      135                      140
```

```
Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
      145                      150                      155                      160
```

Leu Ile Gln Ser Glu Leu
165

<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 47
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cgctgccgag gcgcccgggg acccgcaggc ggccgcgtcc ttgctggccc ctatggacgt 180
gggggaggag ccgctggaga aggcggcgcg cgcgcgact gccaggacc ccaacaccta 240
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tgggttgaaa ccaagctgtg ccaaagaagt taaaagttgc aaaggctcgt gtttcgagag 360
aacatttggg aactgtcgct gtgatgtgc ctgtgttgag cttggaaact gctgtttaga 420
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<210> 48

<211> 925

<212> PRT

<213> Homo sapiens

<400> 48

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35 40 45

Leu Leu Ala Pro Met Asp Val Gly Glu Glu Pro Leu Glu Lys Ala Ala
50 55 60

Arg Ala Arg Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu
65 70 75 80

Val Leu Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly
85 90 95

Leu Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
 100 105 110

Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val Glu
 115 120 125

Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu Pro Glu
 130 135 140

His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys Arg Leu Thr
 145 150 155 160

Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp Lys Gly Asp Cys
 165 170 175

Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu Lys Ser Trp Val Glu
 180 185 190

Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln Cys Pro Ala Gly Phe Glu
 195 200 205

Thr Pro Pro Thr Leu Leu Phe Ser Leu Asp Gly Phe Arg Ala Glu Tyr
 210 215 220

Leu His Thr Trp Gly Gly Leu Leu Pro Val Ile Ser Lys Leu Lys Lys
 225 230 235 240

Cys Gly Thr Tyr Thr Lys Asn Met Arg Pro Val Tyr Pro Thr Lys Thr
 245 250 255

Phe Pro Asn His Tyr Ser Ile Val Thr Gly Leu Tyr Pro Glu Ser His
 260 265 270

Gly Ile Ile Asp Asn Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe
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Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
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Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
 305 310 315 320

Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
 325 330 335

Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
 340 345 350

Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr
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 Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
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 Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
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 Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
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 Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
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 Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
 465 470 475 480
 Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
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 Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
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 Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
 515 520 525
 Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
 530 535 540
 Gln Ala Leu Phe Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu
 545 550 555 560
 Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
 565 570 575
 Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
 580 585 590
 His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
 595 600 605

His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
 610 615 620

Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr
 625 630 635 640

Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
 645 650 655

Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
 660 665 670

Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
 675 680 685

Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
 690 695 700

Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
 705 710 715 720

Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
 725 730 735

Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
 740 745 750

Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
 755 760 765

Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
 770 775 780

Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
 785 790 795 800

Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
 805 810 815

Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
 820 825 830

Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
 835 840 845

Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
 850 855 860

Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
865 870 875 880

Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
885 890 895

Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu
900 905 910

Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
915 920 925

<210> 49

<211> 2709

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 299

<212> PRT

<213> Homo sapiens

<400> 50

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35 40 45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
50 55 60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
65 70 75 80

Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
85 90 95

Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
100 105 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
115 120 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Val Leu His Val
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Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
 145 150 155 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
 165 170 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
 180 185 190

Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
 195 200 205

Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
 210 215 220

Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
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Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
 245 250 255

Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
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Asn Asn Val Lys Pro Arg Lys Leu Arg Lys Asp
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<210> 51

<211> 1019

<212> DNA

<213> Homo sapiens

<400> 51

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<210> 52

<211> 1332

<212> DNA

<213> Homo sapiens

<400> 52

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<210> 53

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (3)

<223> "Xaa" at position 3 can be any amino acid

<220>

<223> Description of Artificial Sequence: Cytokine
receptor extracellular motif found in many
species.

<400> 53

Trp Ser Xaa Trp Ser

1

5